

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 29, 2002, 08:24:26 ; Search time 64.65 Seconds

(without alignments)
34.185 Million cell updates/sec

Title: US-09-787-097-12_COPY_1279_1301
Sequence: 1 LVQFVFVFSCFSLSLVAAVVM 23

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR.71:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	719	2 T00266	hypothetical prote
2	67	57.8	1291	2 T21694	hypothetical prote
3	56	48.3	1737	2 T00209	MEG8 protein - hu
4	53	45.7	700	2 B84125	iron-sulphur-bind
5	52	44.8	150	2 S47459	probable membrane
6	52	44.8	434	2 AG0690	two component sens
7	51	44.0	273	2 A72378	conserved hypothet
8	50	43.1	430	2 B81263	probable ABC trans
9	50	43.1	433	2 C64917	terminator region
10	50	43.1	433	2 C90918	sensor histidine p
11	50	43.1	433	2 H85766	hypothetical prote
12	49.5	42.7	336	2 AH1212	TN16 ORF14 and to
13	49	42.2	262	2 S59078	conserved hypothet
14	49	42.2	387	2 G70337	Na+/H+-exchanging
15	48	41.4	180	2 B88134	hypothetical prote
16	48	41.4	180	2 AH3153	glycosyl transfera
17	48	41.4	320	2 A95187	hypothetical prote
18	48	41.4	338	1 S44207	sugar ABC transpo
19	48	41.4	344	2 H72418	hypothetical prote
20	48	41.4	366	2 S74387	hypothetical prote
21	48	41.4	379	2 AB2423	probable ABC trans
22	47.5	40.9	705	2 DB4680	trax protein - Esc
23	47	40.5	248	2 J01338	hypothetical prote
24	47	40.5	295	2 T16231	hypothetical prote
25	47	40.5	308	2 T24912	hypothetical prote
26	47	40.5	320	2 S65078	beta-carotene keto
27	47	40.5	347	2 A90318	hypothetical prote
28	47	40.5	352	2 A95098	hypothetical prote
29	47	40.5	360	2 A84944	hypothetical prote

30	47	40.5	361	2 E97965	hypothetical prote
31	47	40.5	364	2 D96973	spore germination
32	47	40.5	555	2 T17320	hypothetical prote
33	47	40.5	697	2 T18681	hypothetical prote
34	46.5	40.1	161	2 T20676	hypothetical prote
35	46.5	40.1	177	1 C64067	probable protein-d
36	46.5	40.1	267	2 D97565	transport protein
37	46.5	40.1	267	2 AB2786	SRG-independent pr
38	46.5	40.1	628	2 A99317	conserved hypothet
39	46	39.7	224	1 PWF65	H+-transporting tw
40	46	39.7	363	2 B98054	glycosyl transfera
41	46	39.7	365	2 T33499	hypothetical prote
42	46	39.7	387	2 T49246	D4 dopamine recept
43	46	39.7	439	2 T50688	proline transport
44	46	39.7	1539	2 T30037	hypothetical prote
45	45	38.8	150	2 T12547	hypothetical prote

ALIGNMENTS

RESULT 1
T00266
hypothetical protein KIAA0534 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence-revision 01-Feb-1999 #text-change 21-Jul-2000
C:Accession: T00266
R:Nagase, T., Ishikawa, K., Miyajima, N., Tanaka, A., Kotani, H., Nomura, N., Ohara,
DNA Res. 5, 31-39, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. IX. The comp
A:Reference number: Z14086; MUID:98290545
A:Accession: T00266
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-719 <NAC>
A:Cross-references: EMBL:AB011106; NID:93043591; PIDN:BA025460.1; PID:93043592
A:Experimental source: brain
C:Genetics:
A:Note: KIAA0534

Query Match
Best Local Similarity 100.0%; Score 116; DB 2; Length 719;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVQFVFVFSCFSLSLVAAVVM 23
DB 570 LVQFVFVFSCFSLSLVAAVVM 592

RESULT 2
T21694
hypothetical protein F33C8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 18-Feb-2000
C:Accession: T21694
R:Percy, C
submitted to the EMBL Data Library, February 1996
A:Reference number: Z19460
A:Accession: T21694
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1291 <WII>
A:Cross-references: EMBL:669790; PIDN:CA093653.1; GSPDB:GN00028; CESP:F33C8.1
C:Experimental source: clone F33C8
C:Genetics:
A:Gene: CESP:F33C8.1
A:Map position: X
A:Introns: 18/3; 61/3; 99/2; 128/3; 166/2; 204/2; 352/3; 439/1; 467/3; 549/1; 597/1;

Query Match
Best Local Similarity 57.8%; Score 67; DB 2; Length 1291;
54.5%; Pred. No. 0.14;